Amendments to the Claims

This listing of claims replaces all prior versions, and listings, of the claims in the application.

Listing of Claims:

Claims 1-115 (Canceled)

116. (Currently Amended) A detection probe for use in determining the presence of SARS-CoV in a test sample, said probe comprising a target binding portion having a base sequence which consists of or is contained within and includes at least 18 contiguous bases ~~that is perfectly complementary to all or a portion of a target sequence consisting~~ of ~~the~~ a base sequence selected from the group consisting of SEQ ID NO:3, ~~or~~ its complement, and the DNA equivalents thereof,

wherein said target binding [[region]] portion forms a hybrid stable for detection with said target sequence under stringent hybridization conditions,

wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions, and

wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions.

Claims 117-123 (Canceled)

124. (Currently Amended) The probe of claim 116, wherein the base sequence of said ~~probe is perfectly complementary to all or a portion~~ target binding portion consists of [[the]] a base sequence selected from the group consisting of SEQ ID NO:3, [[or]] its complement, and the DNA equivalents thereof.

125. (Currently Amended) The probe of claim 116, wherein the base sequence of said probe ~~is perfectly complementary to 18 to 23 contiguous bases of the~~ consists of a base sequence selected from the group consisting of SEQ ID NO:3, [[or]] its complement, and the DNA equivalents thereof.

126. (Previously Presented) The probe of claim 116, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

127. (Previously Presented) The probe of claim 126, wherein said probe comprises a pair of interacting labels.

128. (Previously Presented) The probe of claim 127, wherein said pair of interacting labels is selected from the group consisting of a luminescent/quencher pair, a luminescent/adduct pair, a Förrester energy transfer pair and a dye dimer.

129. (Previously Presented) The probe of claim 116, wherein said probe comprises a detectable label.

130. (Previously Presented) The probe of claim 116, wherein said conditions include a temperature of about 60°C and a salt concentration of about 0.6 M to about 0.9 M.

131. (Withdrawn) A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said probe of claim 116 under said conditions; and

b) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

Claims 132-138 (Canceled)

139. (Withdrawn - Currently Amended) The method of claim 131, wherein the base sequence of said ~~probe is perfectly complementary to all or a portion~~ target binding portion consists of [[the]] a base sequence selected from the group consisting of SEQ ID NO:3, [[or]] its complement, and the DNA equivalents thereof.

140. (Withdrawn - Currently Amended) The method of claim 131, wherein the base sequence of said probe ~~is perfectly complementary to 18 to 23 contiguous bases of the~~ consists of a base sequence selected from the group consisting of SEQ ID NO:3, [[or]] its complement, and the DNA equivalents thereof.

141. (Withdrawn) The method of claim 131, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

142. (Withdrawn) The method of claim 141, wherein said probe comprises a pair of interacting labels.

143. (Withdrawn) The method of claim 142, wherein said pair of interacting labels is selected from the group consisting of a luminescent/quencher pair, a luminescent/adduct pair, a Förrester energy transfer pair and a dye dimer.

144. (Withdrawn) The method of claim 131, wherein said probe comprises a detectable label.

Claims 145-152 (Canceled)

153. (Withdrawn - Currently Amended) A method of amplifying a target region present in SARS-CoV nucleic acid, said method comprising the steps of:

a) contacting a test sample with ~~said~~ a set of ~~claim 145~~ amplification oligonucleotides comprising: (i) a first oligonucleotide, the base sequence of which is contained within and includes at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:24, the DNA equivalent thereof, and either of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and (ii) a second oligonucleotide, the base sequence of which is contained within and includes at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:25, the DNA equivalent thereof, and either of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

b) exposing said test sample to isothermal amplification conditions such that said target region, if present in said test sample, is amplified.

Claims 154-159 (Canceled)

160. (Withdrawn - Currently Amended) The method of claim [[159]] 153, wherein at least one of said first and second oligonucleotides comprises a T7 promoter sequence.

161. (Withdrawn - Currently Amended) ~~A~~ The method ~~for determining the presence of SARS-CoV in a test sample, said method~~ of claim 153 further comprising the steps of:

~~a) contacting a test sample with said set of claim 145 under amplification conditions;~~

~~b) amplifying, if present in said test sample, said target region;~~

c) contacting said test sample with a detection probe, said probe ~~being up to 100 bases in length and~~ comprising a target binding portion ~~which forms a hybrid stable for detection with a target sequence contained within or complementary to a sequence contained within said target region under stringent hybridization conditions~~ having a base sequence which consists of or is contained within and includes at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:3, its complement, and the DNA equivalents thereof,

wherein said target binding portion forms a hybrid stable for detection with said target sequence under stringent hybridization conditions,

wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions, and

wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions; and

d) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

Claims 162-169 (Canceled)

170. (Withdrawn - Currently Amended) The method of claim [[162]] 161, wherein the base sequence of said ~~probe is perfectly complementary to all or a portion of the~~ target binding portion consists of a base sequence selected from the group consisting of SEQ ID NO:3, ~~or~~ its complement, and the DNA equivalents thereof.

171. (Withdrawn - Currently Amended) The method of claim [[162]] 161, wherein the base sequence of said probe is ~~perfectly complementary to 18 to 23 contiguous bases of the~~ consists of a base sequence selected from the group consisting of SEQ ID NO:3, ~~or~~ its complement, and the DNA equivalents thereof.

172. (Withdrawn - Currently Amended) The method of claim [[162]] 161, wherein said probe comprises a detectable label.

173. (Withdrawn - Currently Amended) The method of claim 161, wherein said probe is provided to said test sample prior to or during said [[amplifying]] exposing step, such that said target binding region forms a hybrid with said target sequence under the isothermal amplification conditions of said exposing step.

174. (Withdrawn - Currently Amended) The method of claim 161, wherein at least a portion of said determining step occurs during said [[amplifying]] exposing step.

175. (Currently Amended) A kit for use in determining the presence of SARS-CoV in a test sample, said kit comprising:

a first oligonucleotide, the base sequence of which ~~up to 100 bases in length which binds to or extends through a first target sequence~~ is contained within [[the]] and includes at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:24, ~~or~~ the DNA equivalent thereof, and either of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase ~~its complement under amplification conditions~~; and

a second oligonucleotide, the base sequence of which ~~up to 100 bases in length which binds to or extends through a first target sequence~~ is contained within [[the]] and includes at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:25, ~~or~~ the DNA equivalent thereof, and either of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase; and

a detection probe ~~up to 100 bases in length and~~ comprising a target binding portion ~~which forms a hybrid stable for detection with a target sequence contained within the~~ which consists of or

is contained within and includes at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:3, ~~or~~ its complement, and the DNA equivalents thereof,

wherein said target binding region forms a hybrid stable for detection with said target sequence under stringent hybridization conditions,

wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions, and

wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions.

176. (Currently Amended) The ~~probe~~ kit of claim ~~116~~ 175, wherein the base sequence of said target binding portion ~~is perfectly complementary to the~~ consists of a base sequence selected from the group consisting of SEQ ID NO:3, ~~or~~ its complement, and the DNA equivalents thereof.

177. (Currently Amended) The ~~probe~~ kit of claim ~~116~~ 175, wherein the base sequence of said probe ~~is perfectly complementary to the~~ consists of a base sequence selected from the group consisting of SEQ ID NO:3, ~~or~~ its complement, and the DNA equivalents thereof.

Claims 178-181 (Canceled)

182. (New) The method of claim 153, wherein said target region is amplified by a transcription-based amplification.

183. (New) The method of claim 161, wherein said target region is amplified by a transcription-based amplification.